

SEQUENCE LISTING

<110> Myriad Genetics, Inc.

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 Russell, Deanna
 Abkevich, Victor
 Neff, Chris

10 <120> Depression Gene

<130> 1309.03

<160> 3

15 <170> PatentIn version 3.0

<210> 1

<211> 3747

20 <212> DNA
 <213> Homo sapiens

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25 <222> (1) .. (3744)

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gaa aag gac atc aag aca tcc tac atc atg gat cac atg att agt gat
96
Glu Lys Asp Ile Lys Thr Ser Tyr Ile Met Asp His Met Ile Ser Asp
20 25 30
5
gga ttt tta aca ata tca gaa gag gaa aaa gta aga aat gag ccc act
144
Gly Phe Leu Thr Ile Ser Glu Glu Lys Val Arg Asn Glu Pro Thr
35 40 45
10
caa cag caa aga gca gct atg ctg att aaa atg ata ctt aaa aaa gat
192
Gln Gln Gln Arg Ala Ala Met Leu Ile Lys Met Ile Leu Lys Lys Asp
50 55 60
15
aat gat tcc tac gta tca ttc tac aat gct cta cta cat gaa gga tat
240
Asn Asp Ser Tyr Val Ser Phe Tyr Asn Ala Leu Leu His Glu Gly Tyr
65 70 75 80
20
aaa gat ctt gct gcc ctt ctc cat gat ggc att cct gtt gtc tct tct
288
Lys Asp Leu Ala Ala Leu Leu His Asp Gly Ile Pro Val Val Ser Ser
85 90 95
25
tcc agt ggt aaa gat tca gtt agt gga ata act tcg tat gta agg aca
336
Ser Ser Gly Lys Asp Ser Val Ser Gly Ile Thr Ser Tyr Val Arg Thr
100 105 110
30
gtc ctg tgt gaa ggt gga gta cca cag agg cca gtt gtt ttt gtc aca
384
Val Leu Cys Glu Gly Gly Val Pro Gln Arg Pro Val Val Phe Val Thr

115	120	125
agg aag aag ctg gtg aat gca att cag cag aag ctc tcc aaa ttg aaa		
432		
5	Arg Lys Lys Leu Val Asn Ala Ile Gln Gln Lys Leu Ser Lys Leu Lys	
	130	135
		140
ggt gaa cca gga tgg gtc acc ata cat gga atg gca ggc tgt ggg aag		
480		
10	Gly Glu Pro Gly Trp Val Thr Ile His Gly Met Ala Gly Cys Gly Lys	
	145	150
		155
		160
tct gta tta gct gca gaa gct gtt aga gat cat tcc ctt tta gaa ggt		
528		
15	Ser Val Leu Ala Ala Glu Ala Val Arg Asp His Ser Leu Leu Glu Gly	
	165	170
		175
tgt ttc cca ggg gga gtg cat tgg gtt tca gtt ggg aaa caa gac aaa		
576		
20	Cys Phe Pro Gly Gly Val His Trp Val Ser Val Gly Lys Gln Asp Lys	
	180	185
		190
tct ggg ctt ctg atg aaa ctg cag aat ctt tgc aca cgg ttg gat cag		
624		
25	Ser Gly Leu Leu Met Lys Leu Gln Asn Leu Cys Thr Arg Leu Asp Gln	
	195	200
		205
gat gag agt ttt tcc cag agg ctt cca ctt aat att gaa gag gct aaa		
672		
30	Asp Glu Ser Phe Ser Gln Arg Leu Pro Leu Asn Ile Glu Glu Ala Lys	
	210	215
		220

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gac cgt ctc cgc att ctg atg ctt cgc aaa cac cca agg tct ctc ttg
720

Asp Arg Leu Arg Ile Leu Met Leu Arg Lys His Pro Arg Ser Leu Leu
230 235 240
225

5 atc ttg gat gat gtt tgg gac tct tgg gtg ttg aaa gct ttt gac agt
atc ttg gat gat gtt tgg gac tct tgg gtg ttg aaa gct ttt gac agt

768 Ile Leu Asp Asp Val Trp Asp Ser Trp Val Leu Lys Ala Phe Asp Ser
245 250 255

10 cag tgt cag att ctt ctt aca acc aga gac aag agt gtt aca gat tca
cag tgt cag att ctt ctt aca acc aga gac aag agt gtt aca gat tca

816 Gln Cys Gln Ile Leu Leu Thr Thr Arg Asp Lys Ser Val Thr Asp Ser
260 265 270

15 gta atg ggt cct aaa tat gta gtc cct gtg gag agt tcc tta gga aag
gta atg ggt cct aaa tat gta gtc cct gtg gag agt tcc tta gga aag

864 Val Met Gly Pro Lys Tyr Val Val Pro Val Glu Ser Ser Leu Gly Lys
275 280 285

20 gaa aaa gga ctt gaa att tta tcc ctt ttt gtt aat atg aag aag gca
gaa aaa gga ctt gaa att tta tcc ctt ttt gtt aat atg aag aag gca

912 Glu Lys Gly Leu Glu Ile Leu Ser Leu Phe Val Asn Met Lys Lys Ala
290 295 300

25 gat ttg cca gaa caa gct cat agt att ata aaa gaa tgt aaa ggc tct
gat ttg cca gaa caa gct cat agt att ata aaa gaa tgt aaa ggc tct

960 Asp Leu Pro Glu Gln Ala His Ser Ile Ile Lys Glu Cys Lys Gly Ser
305 310 315 320

30 ccc ctt gta gta tct tta att ggt gca ctt tta cgt gat ttt ccc aat
ccc ctt gta gta tct tta att ggt gca ctt tta cgt gat ttt ccc aat

1008 Pro Leu Val Val Ser Leu Ile Gly Ala Leu Leu Arg Asp Phe Pro Asn
Pro Leu Val Val Ser Leu Ile Gly Ala Leu Leu Arg Asp Phe Pro Asn

	325	330	335
cgc tgg gag tac tac ctc aaa cag ctt cag aat aag cag ttt aag aga			
1056			
5	Arg Trp Glu Tyr Tyr Leu Lys Gln Leu Gln Asn Lys Gln Phe Lys Arg		
	340	345	350
ata agg aaa tct tcg tct tat gat tat gag gct cta gat gaa gcc atg			
1104			
10	Ile Arg Lys Ser Ser Ser Tyr Asp Tyr Glu Ala Leu Asp Glu Ala Met		
	355	360	365
tct ata agt gtt gaa atg ctc aga gaa gac atc aaa gat tat tac aca			
1152			
15	Ser Ile Ser Val Glu Met Leu Arg Glu Asp Ile Lys Asp Tyr Tyr Thr		
	370	375	380
gat ctt tcc atc ctt cag aag gac gtt aag gtg cct aca aag gtg tta			
1200			
20	Asp Leu Ser Ile Leu Gln Lys Asp Val Lys Val Pro Thr Lys Val Leu		
	385	390	395
			400
tgt att ctc tgg gac atg gaa act gaa gaa gtt gaa gac ata ctg cag			
1248			
25	Cys Ile Leu Trp Asp Met Glu Thr Glu Glu Val Glu Asp Ile Leu Gln		
	405	410	415
gag ttt gta aat aag tct ctt tta ttc tgt gat cgg aat gga aag tcg			
1296			
30	Glu Phe Val Asn Lys Ser Leu Leu Phe Cys Asp Arg Asn Gly Lys Ser		
	420	425	430

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ttt cgt tat tat tta cat gat ctt caa gta gat ttt ctt aca gag aag
1344

Phe Arg Tyr Tyr Leu His Asp Leu Gln Val Asp Phe Leu Thr Glu Lys
435 440 445

5 aat tgc agc cag ctt cag gat cta cat aag aag ata atc act cag ttt
aat tgc agc cag ctt cag gat cta cat aag aag ata atc act cag ttt

1392 Asn Cys Ser Gln Leu Gln Asp Leu His Lys Lys Ile Ile Thr Gln Phe
450 455 460

10 cag aga tat cac cag ccg cat act ctt tca cca gat cag gaa gac tgt
cag aga tat cac cag ccg cat act ctt tca cca gat cag gaa gac tgt

1440 Gln Arg Tyr His Gln Pro His Thr Leu Ser Pro Asp Gln Glu Asp Cys
465 470 475 480

15 atg tat tgg tac aac ttt ctg gcc tat cac atg gcc agt gcc aag atg
atg tat tgg tac aac ttt ctg gcc tat cac atg gcc agt gcc aag atg

1488 Met Tyr Trp Tyr Asn Phe Leu Ala Tyr His Met Ala Ser Ala Lys Met
485 490 495

20 cac aag gaa ctt tgt gct tta atg ttt tcc ctg gat tgg att aaa gca
cac aag gaa ctt tgt gct tta atg ttt tcc ctg gat tgg att aaa gca

1536 His Lys Glu Leu Cys Ala Leu Met Phe Ser Leu Asp Trp Ile Lys Ala
500 505 510

25 aaa aca gaa ctt gta ggc cct gct cat ctg att cat gaa ttt gtg gaa
aaa aca gaa ctt gta ggc cct gct cat ctg att cat gaa ttt gtg gaa

1584 Lys Thr Glu Leu Val Gly Pro Ala His Leu Ile His Glu Phe Val Glu
515 520 525

30 tac aga cat ata cta gat gaa aag gat tgt gca gtc agt gag aat ttt
tat aga cat ata cta gat gaa aag gat tgt gca gtc agt gag aat ttt

1632 Tyr Arg His Ile Leu Asp Glu Lys Asp Cys Ala Val Ser Glu Asn Phe
Tyr Arg His Ile Leu Asp Glu Lys Asp Cys Ala Val Ser Glu Asn Phe

	530	535	540
	cag gag ttt tta tct tta aat gga cac ctt ctt gga cga cag cca ttt		
	1680		
5	Gln Glu Phe Leu Ser Leu Asn Gly His Leu Leu Gly Arg Gln Pro Phe		
	545	550	555
	cct aat att gta caa ctg ggt ctc tgt gag ccg gaa act tca gaa gtt		
	1728		
10	Pro Asn Ile Val Gln Leu Gly Leu Cys Glu Pro Glu Thr Ser Glu Val		
	565	570	575
	tat cag caa gct aag ctg cag gcc aag cag gag gtc gat aat gga atg		
	1776		
15	Tyr Gln Gln Ala Lys Leu Gln Ala Lys Gln Glu Val Asp Asn Gly Met		
	580	585	590
	ctt tac ctg gaa tgg ata aac aaa aaa aac atc acg aat ctt tcc cgc		
	1824		
20	Leu Tyr Leu Glu Trp Ile Asn Lys Lys Asn Ile Thr Asn Leu Ser Arg		
	595	600	605
	tta gtt gtc cgc ccc cac aca gat gct gtt tac cat gcc tgc ttt tct		
	1872		
25	Leu Val Val Arg Pro His Thr Asp Ala Val Tyr His Ala Cys Phe Ser		
	610	615	620
	gag gat ggt cag aga ata gct tct tgt gga gct gat aaa acc tta cag		
	1920		
30	Glu Asp Gly Gln Arg Ile Ala Ser Cys Gly Ala Asp Lys Thr Leu Gln		
	625	630	635
	640		

gtg ttc aaa gct gaa aca gga gag aaa ctt cta gaa atc aag gct cat
1968

Val Phe Lys Ala Glu Thr Gly Glu Lys Leu Leu Glu Ile Lys Ala His
645 650 655

5

gag gat gaa gtg ctt tgt tgt gca ttc tct aca gat gac aga ttt ata
2016

Glu Asp Glu Val Leu Cys Cys Ala Phe Ser Thr Asp Asp Arg Phe Ile
660 665 670

10

gca acc tgc tca gtg gat aaa aaa gtg aag att tgg aat tct atg act
2064

Ala Thr Cys Ser Val Asp Lys Lys Val Lys Ile Trp Asn Ser Met Thr
675 680 685

15

. ggg gaa cta gta cac acc tat gat gag cac tca gag caa gtc aat tgc
2112

Gly Glu Leu Val His Thr Tyr Asp Glu His Ser Glu Gln Val Asn Cys
690 695 700

20

tgc cat ttc acc aac agt agt cat cat ctt ctc tta gcc act ggg tca
2160

Cys His Phe Thr Asn Ser Ser His His Leu Leu Leu Ala Thr Gly Ser
705 710 715 720

25

agt gac tgc ttc ctc aaa ctt tgg gat ttg aat caa aaa gaa tgt cga
2208

Ser Asp Cys Phe Leu Lys Leu Trp Asp Leu Asn Gln Lys Glu Cys Arg
725 730 735

30

aat acc atg ttt ggt cat aca aat tca gtc aat cac tgc aga ttt tca
2256

Asn Thr Met Phe Gly His Thr Asn Ser Val Asn His Cys Arg Phe Ser

	740	745	750
	cca gat gat aag ctt ttg gct agt tgt tca gct gat gga acc tta aag		
	2304		
5	Pro Asp Asp Lys Leu Leu Ala Ser Cys Ser Ala Asp Gly Thr Leu Lys		
	755	760	765
	ctt tgg gat gcg aca tca gca aat gag agg aaa agc att aat gtg aaa		
	2352		
10	Leu Trp Asp Ala Thr Ser Ala Asn Glu Arg Lys Ser Ile Asn Val Lys		
	770	775	780
	cag ttc ttc cta aat ttg gag gac cct caa gag gat atg gaa gtg ata		
	2400		
15	Gln Phe Phe Leu Asn Leu Glu Asp Pro Gln Glu Asp Met Glu Val Ile		
	785	790	795
	gtg aag tgt tgt tcg tgg tct gct gat ggt gca agg ata atg gtg gca		
	2448		
20	Val Lys Cys Cys Ser Trp Ser Ala Asp Gly Ala Arg Ile Met Val Ala		
	805	810	815
	gca aaa aat aaa atc ttt ctt ttt gac att cat act agt ggc cta ttg		
	2496		
25	Ala Lys Asn Lys Ile Phe Leu Phe Asp Ile His Thr Ser Gly Leu Leu		
	820	825	830
	gga gaa atc cac acg ggc cat cac agc acc atc cag tac tgt gac ttc		
	2544		
30	Gly Glu Ile His Thr Gly His His Ser Thr Ile Gln Tyr Cys Asp Phe		
	835	840	845

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tcc cca caa aac cat ttg gca gtg gtt gct ttg tcc cag tac tgt gta
2592
Ser Pro Gln Asn His Leu Ala Val Val Ala Leu Ser Gln Tyr Cys Val
850 855 860
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gag ttg tgg aat aca gac tca cgt tca aag gtg gct gat tgc aga gga
2640
Glu Leu Trp Asn Thr Asp Ser Arg Ser Lys Val Ala Asp Cys Arg Gly
865 870 875 880
10
cat tta agt tgg gtt cat ggt gtg atg ttt tct cct gat gga tca tca
2688
His Leu Ser Trp Val His Gly Val Met Phe Ser Pro Asp Gly Ser Ser
885 890 895
15
ttt ttg aca tct tct gat gac cag aca atc agg ctc tgg gag aca aag
2736
Phe Leu Thr Ser Ser Asp Asp Gln Thr Ile Arg Leu Trp Glu Thr Lys
900 905 910
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aaa gta tgt aag aac tct gct gta atg tta aag caa gaa gta gat gtt
2784
Lys Val Cys Lys Asn Ser Ala Val Met Leu Lys Gln Glu Val Asp Val
915 920 925
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gtg ttt caa gaa aat gaa gtg atg gtc ctt gca gtt gac cat ata aga
2832
Val Phe Gln Glu Asn Glu Val Met Val Leu Ala Val Asp His Ile Arg
930 935 940
30
cgt ctg caa ctc att aat gga aga aca ggt cag att gat tat ctg act
2880
Arg Leu Gln Leu Ile Asn Gly Arg Thr Gly Gln Ile Asp Tyr Leu Thr

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945 950 955 960
gaa gct caa gtt agc tgc tgt tgc tta agt cca cat ctt cag tac att
2928
5 Glu Ala Gln Val Ser Cys Cys Cys Leu Ser Pro His Leu Gln Tyr Ile
965 970 975
gca ttt gga gat gaa aat gga gcc att gag att tta gaa ctt gta aac
2976
10 Ala Phe Gly Asp Glu Asn Gly Ala Ile Glu Ile Leu Glu Leu Val Asn
980 985 990
aat aga atc ttc cag tcc agg ttt cag cac aag aaa act gta tgg
cac 3024
15 Asn Arg Ile Phe Gln Ser Arg Phe Gln His Lys Lys Thr Val Trp
His
995 1000 1005
atc cag ttc aca gcc gat gag aag act ctt att tca agt tct gat
20 3069
Ile Gln Phe Thr Ala Asp Glu Lys Thr Leu Ile Ser Ser Ser Asp
1010 1015 1020
gat gct gaa att cag gta tgg aat tgg caa ttg gac aaa tgt atc
25 3114
Asp Ala Glu Ile Gln Val Trp Asn Trp Gln Leu Asp Lys Cys Ile
1025 1030 1035
ttt cta cga ggc cat cag gaa aca gtg aaa gac ttt aga ctc ttg
30 3159
Phe Leu Arg Gly His Gln Glu Thr Val Lys Asp Phe Arg Leu Leu
1040 1045 1050

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aaa aat tca aga ctg ctt tct tgg tca ttt gat gga aca gtg aag
3204 Lys Asn Ser Arg Leu Leu Ser Trp Ser Phe Asp Gly Thr Val Lys
1055 1060 1065

5 gta tgg aat att att act gga aat aaa gaa aaa gac ttt gtc tgt
3249 Val Trp Asn Ile Ile Thr Gly Asn Lys Glu Lys Asp Phe Val Cys
1070 1075 1080

10 cac cag ggt aca gta ctt tct tgt gac att tct cac gat gct acc
3294 His Gln Gly Thr Val Leu Ser Cys Asp Ile Ser His Asp Ala Thr
1085 1090 1095

15 aag ttt tca tct acc tct gct gac aag act gca aag atc tgg agt
3339 Lys Phe Ser Ser Thr Ser Ala Asp Lys Thr Ala Lys Ile Trp Ser
1100 1105 1110

20 ttt gat ctc ctt ttg cca ctt cat gaa ttg agg ggc cac aac ggc
3384 Phe Asp Leu Leu Leu Pro Leu His Glu Leu Arg Gly His Asn Gly
1115 1120 1125

25 tgt gtg cgc tgc tct gcc ttc tct gtg gac agt acc ctg ctg gca
3429 Cys Val Arg Cys Ser Ala Phe Ser Val Asp Ser Thr Leu Leu Ala
1130 1135 1140

30 acg gga gat gac aat gga gaa atc agg ata tgg aat gtc tca aac
3474 Thr Gly Asp Asp Asn Gly Glu Ile Arg Ile Trp Asn Val Ser Asn

1145 1150 1155
ggt gag ctt ctt cat ttg tgt gct ccg ctt tca gaa gaa gga gct
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5 Gly Glu Leu Leu His Leu Cys Ala Pro Leu Ser Glu Glu Gly Ala
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gct acc cat gga ggc tgg gtg act gac ctt tgc ttt tct cca gat
3564
10 Ala Thr His Gly Gly Trp Val Thr Asp Leu Cys Phe Ser Pro Asp
1175 1180 1185
ggc aaa atg ctt atc tct gct gga gga tat att aag tgg tgg aac
3609
15 Gly Lys Met Leu Ile Ser Ala Gly Gly Tyr Ile Lys Trp Trp Asn
1190 1195 1200
gtt gtc act ggg gaa tcc tca cag acc ttc tac aca aat gga acc
3654
20 Val Val Thr Gly Glu Ser Ser Gln Thr Phe Tyr Thr Asn Gly Thr
1205 1210 1215
aat ctt aag aaa ata cac gtg tcc cct gac ttc aaa aca tat gtg
3699
25 Asn Leu Lys Lys Ile His Val Ser Pro Asp Phe Lys Thr Tyr Val
1220 1225 1230
act gtg gat aat ctt ggt att tta tat att tta cag act tta gaa
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1235 1240 1245

taa

3747

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<212> PRT

<213> Homo sapiens

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Gly Phe Leu Thr Ile Ser Glu Glu Lys Val Arg Asn Glu Pro Thr
20 25 30
35 40 45

15
Gly Phe Leu Thr Ile Ser Glu Glu Lys Val Arg Asn Glu Pro Thr
Gly Phe Leu Thr Ile Ser Glu Glu Lys Val Arg Asn Glu Pro Thr
35 40 45
50 55 60
20 25 30

Asn Asp Ser Tyr Val Ser Phe Tyr Asn Ala Leu Leu His Glu Gly Tyr
65 70 75 80

25 Lys Asp Leu Ala Ala Leu Leu His Asp Gly Ile Pro Val Val Ser Ser
85 90 95
20 25 30

Ser Ser Gly Lys Asp Ser Val Ser Gly Ile Thr Ser Tyr Val Arg Thr
100 105 110

30 Val Leu Cys Glu Gly Gly Val Pro Gln Arg Pro Val Val Phe Val Thr
115 120 125
20 25 30

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Arg Lys Lys Leu Val Asn Ala Ile Gln Gln Lys Leu Ser Lys Leu Lys
130 135 140
Gly Glu Pro Gly Trp Val Thr Ile His Gly Met Ala Gly Cys Gly Lys
5 145 150 155 160
Ser Val Leu Ala Ala Glu Ala Val Arg Asp His Ser Leu Leu Glu Gly
165 170 175
10 Cys Phe Pro Gly Gly Val His Trp Val Ser Val Gly Lys Gln Asp Lys
180 185 190
Ser Gly Leu Leu Met Lys Leu Gln Asn Leu Cys Thr Arg Leu Asp Gln
195 200 205
15 Asp Glu Ser Phe Ser Gln Arg Leu Pro Leu Asn Ile Glu Glu Ala Lys
210 215 220
Asp Arg Leu Arg Ile Leu Met Leu Arg Lys His Pro Arg Ser Leu Leu
20 225 230 235 240
Ile Leu Asp Asp Val Trp Asp Ser Trp Val Leu Lys Ala Phe Asp Ser
245 250 255
25 Gln Cys Gln Ile Leu Leu Thr Thr Arg Asp Lys Ser Val Thr Asp Ser
260 265 270
Val Met Gly Pro Lys Tyr Val Val Pro Val Glu Ser Ser Leu Gly Lys
275 280 285
30 Glu Lys Gly Leu Glu Ile Leu Ser Leu Phe Val Asn Met Lys Lys Ala
290 295 300

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Asp Leu Pro Glu Gln Ala His Ser Ile Ile Lys Glu Cys Lys Gly Ser
305 310 315 320

Pro Leu Val Val Ser Leu Ile Gly Ala Leu Leu Arg Asp Phe Pro Asn
5 325 330 335

Arg Trp Glu Tyr Tyr Leu Lys Gln Leu Gln Asn Lys Gln Phe Lys Arg
340 345 350

Ile Arg Lys Ser Ser Ser Tyr Asp Tyr Glu Ala Leu Asp Glu Ala Met
10 355 360 365

Ser Ile Ser Val Glu Met Leu Arg Glu Asp Ile Lys Asp Tyr Tyr Thr
370 375 380

Asp Leu Ser Ile Leu Gln Lys Asp Val Lys Val Pro Thr Lys Val Leu
15 385 390 395 400

Cys Ile Leu Trp Asp Met Glu Thr Glu Glu Val Glu Asp Ile Leu Gln
20 405 410 415

Glu Phe Val Asn Lys Ser Leu Leu Phe Cys Asp Arg Asn Gly Lys Ser
420 425 430

Phe Arg Tyr Tyr Leu His Asp Leu Gln Val Asp Phe Leu Thr Glu Lys
25 435 440 445

Asn Cys Ser Gln Leu Gln Asp Leu His Lys Lys Ile Ile Thr Gln Phe
450 455 460

Gln Arg Tyr His Gln Pro His Thr Leu Ser Pro Asp Gln Glu Asp Cys
30 465 470 475 480

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Met Tyr Trp Tyr Asn Phe Leu Ala Tyr His Met Ala Ser Ala Lys Met
485 490 495
His Lys Glu Leu Cys Ala Leu Met Phe Ser Leu Asp Trp Ile Lys Ala
500 505 510
Lys Thr Glu Leu Val Gly Pro Ala His Leu Ile His Glu Phe Val Glu
515 520 525
10 Tyr Arg His Ile Leu Asp Glu Lys Asp Cys Ala Val Ser Glu Asn Phe
530 535 540
Gln Glu Phe Leu Ser Leu Asn Gly His Leu Leu Gly Arg Gln Pro Phe
545 550 555 560
15 Pro Asn Ile Val Gln Leu Gly Leu Cys Glu Pro Glu Thr Ser Glu Val
565 570 575
Tyr Gln Gln Ala Lys Leu Gln Ala Lys Gln Glu Val Asp Asn Gly Met
20 580 585 590
Leu Tyr Leu Glu Trp Ile Asn Lys Asn Ile Thr Asn Leu Ser Arg
595 600 605
25 Leu Val Val Arg Pro His Thr Asp Ala Val Tyr His Ala Cys Phe Ser
610 615 620
Glu Asp Gly Gln Arg Ile Ala Ser Cys Gly Ala Asp Lys Thr Leu Gln
625 630 635 640
30 Val Phe Lys Ala Glu Thr Gly Glu Lys Leu Leu Glu Ile Lys Ala His
645 650 655

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Glu Asp Glu Val Leu Cys Cys Ala Phe Ser Thr Asp Asp Arg Phe Ile
660 665 670
Ala Thr Cys Ser Val Asp Lys Lys Val Lys Ile Trp Asn Ser Met Thr
675 680 685
5
Gly Glu Leu Val His Thr Tyr Asp Glu His Ser Glu Gln Val Asn Cys
690 695 700
Ser Asp Cys Phe Leu Lys Leu Trp Asp Leu Asn Gln Lys Glu Cys Arg
705 710 715 720
10 Cys His Phe Thr Asn Ser Ser His His Leu Leu Leu Ala Thr Gly Ser
725 730 735
Asn Thr Met Phe Gly His Thr Asn Ser Val Asn His Cys Arg Phe Ser
740 745 750
15 Pro Asp Asp Lys Leu Leu Ala Ser Cys Ser Ala Asp Gly Thr Leu Lys
755 760 765
20 Leu Trp Asp Ala Thr Ser Ala Asn Glu Arg Lys Ser Ile Asn Val Lys
770 775 780
25 Gln Phe Phe Leu Asn Leu Glu Asp Pro Gln Glu Asp Met Glu Val Ile
785 790 795 800
Val Lys Cys Cys Ser Trp Ser Ala Asp Gly Ala Arg Ile Met Val Ala
805 810 815
30 Ala Lys Asn Lys Ile Phe Leu Phe Asp Ile His Thr Ser Gly Leu Leu
820 825 830

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Gly Glu Ile His Thr Gly His His Ser Thr Ile Gln Tyr Cys Asp Phe
835 840 845

Ser Pro Gln Asn His Leu Ala Val Val Ala Leu Ser Gln Tyr Cys Val
5 850 855 860

Glu Leu Trp Asn Thr Asp Ser Arg Ser Lys Val Ala Asp Cys Arg Gly
865 870 875 880

10 His Leu Ser Trp Val His Gly Val Met Phe Ser Pro Asp Gly Ser Ser
885 890 895

Phe Leu Thr Ser Ser Asp Asp Gln Thr Ile Arg Leu Trp Glu Thr Lys
900 905 910

15 Lys Val Cys Lys Asn Ser Ala Val Met Leu Lys Gln Glu Val Asp Val
915 920 925

Val Phe Gln Glu Asn Glu Val Met Val Leu Ala Val Asp His Ile Arg
20 930 935 940

Arg Leu Gln Leu Ile Asn Gly Arg Thr Gly Gln Ile Asp Tyr Leu Thr
945 950 955 960

25 Glu Ala Gln Val Ser Cys Cys Cys Leu Ser Pro His Leu Gln Tyr Ile
965 970 975

Ala Phe Gly Asp Glu Asn Gly Ala Ile Glu Ile Leu Glu Leu Val Asn
980 985 990

30 Asn Arg Ile Phe Gln Ser Arg Phe Gln His Lys Lys Thr Val Trp
His 995 1000 1005

Ile Gln Phe Thr Ala Asp Glu Lys Thr Leu Ile Ser Ser Ser Asp
1010 1015 1020

5 Asp Ala Glu Ile Gln Val Trp Asn Trp Gln Leu Asp Lys Cys Ile
1025 1030 1035

phe Leu Arg Gly His Gln Glu Thr Val Lys Asp Phe Arg Leu Leu
1040 1045 1050

10 Lys Asn Ser Arg Leu Leu Ser Trp Ser Phe Asp Gly Thr Val Lys
1055 1060 1065

Val Trp Asn Ile Ile Thr Gly Asn Lys Glu Lys Asp Phe Val Cys
1070 1075 1080

15 His Gln Gly Thr Val Leu Ser Cys Asp Ile Ser His Asp Ala Thr
1085 1090 1095

20 Lys Phe Ser Ser Thr Ser Ala Asp Lys Thr Ala Lys Ile Trp Ser
1100 1105 1110

Phe Asp Leu Leu Leu Pro Leu His Glu Leu Arg Gly His Asn Gly
1115 1120 1125

25 Cys Val Arg Cys Ser Ala Phe Ser Val Asp Ser Thr Leu Leu Ala
1130 1135 1140

Thr Gly Asp Asp Asn Gly Glu Ile Arg Ile Trp Asn Val Ser Asn
1145 1150 1155

30 Gly Glu Leu Leu His Leu Cys Ala Pro Leu Ser Glu Glu Gly Ala
1160 1165 1170

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Ala Thr His Gly Gly Trp Val Thr Asp Leu Cys Phe Ser Pro Asp
1175 1180 1185
5 Gly Lys Met Leu Ile Ser Ala Gly Gly Tyr Ile Lys Trp Trp Asn
1190 1195 1200
Val Val Thr Gly Glu Ser Ser Gln Thr Phe Tyr Thr Asn Gly Thr
1205 1210 1215
10 Asn Leu Lys Lys Ile His Val Ser Pro Asp Phe Lys Thr Tyr Val
1220 1225 1230
Thr Val Asp Asn Leu Gly Ile Leu Tyr Ile Leu Gln Thr Leu Glu
1235 1240 1245
15 <210> 3
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<212> PRT
20 <213> Homo sapiens

<400> 3
Met Asp Ala Lys Ala Arg Asn Cys Leu Leu Gln His Arg Glu Ala Leu
1 5 10 15
Glu Lys Asp Ile Lys Thr Ser Tyr Ile Met Asp His Met Ile Ser Asp
25 20 25 30
30 Gly Phe Leu Thr Ile Ser Glu Glu Lys Val Arg Asn Glu Pro Thr
35 40 45
Gln Gln Gln Arg Ala Ala Met Leu Ile Lys Met Ile Leu Lys Lys Asp
50 55 60

Asn Asp Ser Tyr Val Ser Phe Tyr Asn Ala Leu Leu His Glu Gly Tyr
Asn Asp Ser Tyr Val Ser Phe Tyr Asn Ala Leu Leu His Glu Gly Tyr
65 70 75 80
Lys Asp Leu Ala Ala Leu Leu His Asp Gly Ile Pro Val Val Ser Ser
5 85 90 95
Ser Ser Gly Lys Asp Ser Val Ser Gly Ile Thr Ser Tyr Val Arg Thr
100 105 110
Val Leu Cys Glu Gly Gly Val Pro Gln Arg Pro Val Val Phe Val Thr
115 120 125
Arg Lys Lys Leu Val Asn Ala Ile Gln Gln Lys Leu Ser Lys Leu Lys
15 130 135 140
Gly Glu Pro Gly Trp Val Thr Ile His Gly Met Ala Gly Cys Gly Lys
145 150 155 160
Ser Val Leu Ala Ala Glu Ala Val Arg Asp His Ser Leu Leu Glu Gly
20 165 170 175
Cys Phe Pro Gly Gly Val His Trp Val Ser Val Gly Lys Gln Asp Lys
180 185 190
Ser Gly Leu Leu Met Lys Leu Gln Asn Leu Cys Thr Arg Leu Asp Gln
25 195 200 205
Asp Glu Ser Phe Ser Gln Arg Leu Pro Leu Asn Ile Glu Glu Ala Lys
30 210 215 220
Asp Arg Leu Arg Ile Leu Met Leu Arg Lys His Pro Arg Ser Leu Leu
225 230 235 240

Ile Leu Asp Asp Val Trp Asp Ser Trp Val Leu Lys Ala Phe Asp Ser
245 250 255

5 Gln Cys Gln Ile Leu Leu Thr Thr Arg Asp Lys Ser Val Thr Asp Ser
260 265 270

Val Met Gly Pro Lys Tyr Val Val Pro Val Glu Ser Ser Leu Gly Lys
275 280 285

10 Glu Lys Gly Leu Glu Ile Leu Ser Leu Phe Val Asn Met Lys Lys Ala
290 295 300

Asp Leu Pro Glu Gln Ala His Ser Ile Ile Lys Glu Cys Lys Gly Ser
15 305 310 315 320

Pro Leu Val Val Ser Leu Ile Gly Ala Leu Leu Arg Asp Phe Pro Asn
325 330 335

20 Arg Trp Glu Tyr Tyr Leu Lys Gln Leu Gln Asn Lys Gln Phe Lys Arg
340 345 350

Ile Arg Lys Ser Ser Ser Tyr Asp Tyr Glu Ala Leu Asp Glu Ala Met
355 360 365

25 Ser Ile Ser Val Glu Met Leu Arg Glu Asp Ile Lys Asp Tyr Tyr Thr
370 375 380

Asp Leu Ser Ile Leu Gln Lys Asp Val Lys Val Pro Thr Lys Val Leu
385 390 395 400

Cys Ile Leu Trp Asp Met Glu Thr Glu Glu Val Glu Asp Ile Leu Gln
405 410 415

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Glu Phe Val Asn Lys Ser Leu Leu Phe Cys Asp Arg Asn Gly Lys Ser
420 425 430

5 Phe Ser Leu Leu Phe Thr
435

10